

### SEQUENCE LISTING

ı	11	) GE	NERAL	TNFO	RMA	$M \cap T \cap$	
۸		/ GE		TIME O	mm	T + OIA	

- (i) APPLICANT:
  - (A) NAME: UNIVERSITE CATHOLIQUE DE LOUVAIN

Halles Universitaires

- (B) STREET: Place de l' Universite, 1
- (C) CITY: LOUVAIN-LA-NEUVE
- (E) COUNTRY: BELGIUM
- (F) POSTAL CODE (ZIP): B-1348
- (A') NAME: UNIVERSITE DE MONS-HAINAUT
  - (B) STREET: Place du Parc 20
  - (C) CITY: MONS
  - (E) COUNTRY: BELGIUM
  - (F) POSTAL CODE (ZIP): B-7000
- (ii) TITLE OF INVENTION: PEROXISOME-ASSOCIATED PEPTIDE, NUCLEOTIDE SEQUENCE ENCODING SAID PEPTIDE AND THEIR USES IN THE DIAGNOSTIC AND/OR THE TREATMENT OF LUNG INJURIES AND DISEASES, AND OF OXIDATIVE STRESS-RELATED DISORDERS
- (iii) NUMBER OF SEQUENCES: 19
- (iv) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (2) INFORMATION FOR SEO ID NO: 1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 805 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Homo sapiens
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 193..681
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCCAGGAGGC GGAGTGGAAG TGGCCGTGGG GCGGGTATGG GACTAGCTGG CGTGTGCGCC

60

CTGAGACGCT CAGCGGGCTA TATACTCGTC GGTGGGGCCG GCGGTCAGTC TGCGGCAGCG

120





GCAGCAAGAC GGTGCAGTGA AGGAGAGTGG GCGTCTGGCG GGGTCCGCAG TTTCAGCAGA								
GCCGCTGCAG CC ATG GCC CCA ATC AAG GTG GGA GAT GCC ATC CCA GCA  Met Ala Pro Ile Lys Val Gly Asp Ala Ile Pro Ala  1 5 10								
GTG GAG GTG TTT GAA GGG GAG CCA GGG AAC AAG GTG AAC CTG GCA GAG Val Glu Val Phe Glu Gly Glu Pro Gly Asn Lys Val Asn Leu Ala Glu 15 20 25	276							
CTG TTC AAG GGC AAG AAG GGT GTG CTG TTT GGA GTT CCT GGG GCC TTC Leu Phe Lys Gly Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe 30 ,	324							
ACC CCT GGA TGT TCC AAG ACA CAC CTG CCA GGG TTT GTG GAG CAG GCT Thr Pro Gly Cys Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala 45 50 55 60	372							
GAG GCT CTG AAG GCC AAG GGA GTC CAG GTG GTG GCC TGT CTG AGT GTT Glu Ala Leu Lys Ala Lys Gly Val Gln Val Val Ala Cys Leu Ser Val 65 70 75	420							
AAT GAT GCC TTT GTG ACT GGC GAG TGG GGC CGA GCC CAC AAG GCG GAA Asn Asp Ala Phe Val Thr Gly Glu Trp Gly Arg Ala His Lys Ala Glu 80 85 90	468							
GGC AAG GTT CGG CTC CTG GCT GAT CCC ACT GGG GCC TTT GGG AAG GAG Gly Lys Val Arg Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu 95 100 105	516							
ACA GAC TTA TTA CTA GAT GAT TCG CTG GTG TCC ATC TTT GGG AAT CGA Thr Asp Leu Leu Asp Asp Ser Leu Val Ser Ile Phe Gly Asn Arg 110 115 120	564							
CGT CTC AAG AGG TTC TCC ATG GTG GTA CAG GAT GGC ATA GTG AAG GCC Arg Leu Lys Arg Phe Ser Met Val Val Gln Asp Gly Ile Val Lys Ala 135 140	612							
CTG AAT GTG GAA CCA GAT GGC ACA GGC CTC ACC TGC AGC CTG GCA CCC Leu Asn Val Glu Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro 145 150 155	660							
AAT ATC ATC TCA CAG CTC TGA GGCCCTGGGC CAGATTACTT CCTCCACCCC Asn Ile Ile Ser Gln Leu * 160	711							
TCCCTATCTC ACCTGCCCAG CCCTGTGCTG GGGCCCTGCA ATTGGAATGT TGGCCAGATT	771							
TCTGCAATAA ACACTTGTGG TTTGCGGAAA AAAA								

## (2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 163 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:





Met Ala Pro Ile Lys Val Gly Asp Ala Ile Pro Ala Val Glu Val Phe 1 5 10 15

Glu Gly Glu Pro Gly Asn Lys Val Asn Leu Ala Glu Leu Phe Lys Gly 20 25 30

Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr Pro Gly Cys 35 40 45

Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Glu Ala Leu Lys 50 55 60

Ala Lys Gly Val Gln Val Val Ala Cys Leu Ser Val Asn Asp Ala Phe
65 70 75 80

Val Thr Gly Glu Trp Gly Arg Ala His Lys Ala Glu Gly Lys Val Arg 85 90 95

Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu Thr Asp Leu Leu 100 105 110

Leu Asp Asp Ser Leu Val Ser Ile Phe Gly Asn Arg Arg Leu Lys Arg 115 120 125

Phe Ser Met Val Val Gln Asp Gly Ile Val Lys Ala Leu Asn Val Glu 130 135 140

Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn Ile Ile Ser 145 150 155 160

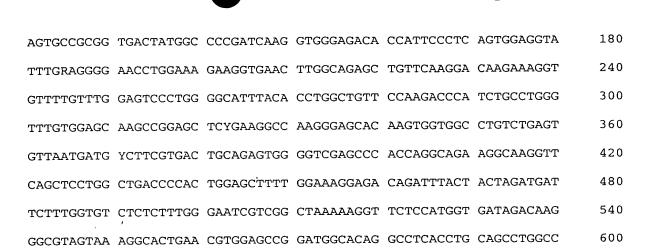
Gln Leu \*

### (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 780 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Rattus Rattus
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 136..624
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGCGTCCTAG GCAGCATAGC CGGATCGGTG CTCCGTGCAT CGGCTACTTG GACGTGCGTG 60

GCAGGCAGAG CAGGCCGGAA AGGAGCAGGT TGGGAGTGTG GTGGGGCCCG CAGCTTCAGC 120



660

720

780

CCCAACATCC TCTCACAACT CTGAGGCCCT GACCAGAATG TCCTCTGACT CTCCCATCTC

CTCCACCCAG CTCTGGGCCA AAGGCCCAGT ACCTCCTTAC CTGAGGGCCA CTGGAATGGA

ACCTTGACAA TATTTCTGCA ATAAACAGTT TAATTTGTGA AAAAAAAAA AAAAAAAAA

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 162 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Rattus Rattus
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION:17
  - (D) OTHER INFORMATION:/product= "Glu or Gly"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION:63
  - (D) OTHER INFORMATION:/product= "Leu or Pro"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 79
  - (D) OTHER INFORMATION:/product= "Ala or Val"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
- Met Ala Pro Ile Lys Val Gly Asp Thr Ile Pro Ser Val Glu Val Phe





Xaa Gly Glu	Pro	Gly	Lys	Lys	Val	Asn	Leu	Ala	Glu	Leu	Phe	Lys	Asp
-	20					25					30		

Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr Pro Gly Cys 35 40 45

Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Gly Ala Xaa Lys 50 55 60

Ala Lys Gly Ala Gln Val Val Ala Cys Leu Ser Val Asn Asp Xaa Phe 65 70 ' 75 80

Val Thr Ala Glu Trp Gly Arg Ala His Gln Ala Glu Gly Lys Val Gln 85 90 95

Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Glu Thr Asp Leu Leu 100 105 110

Leu Asp Asp Ser Leu Val Ser Leu Phe Gly Asn Arg Arg Leu Lys Arg
115 120 125

Phe Ser Met Val Ile Asp Lys Gly Val Val Lys Ala Leu Asn Val Glu 130 135 140

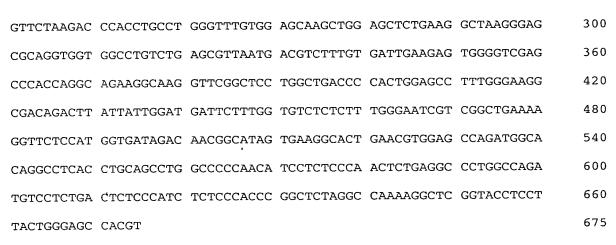
Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn Ile Leu Ser 145 150 155 160

Gln Leu

## (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 675 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Mouse
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 99..588
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

60	GGTTGGGAGT	GAAAGAAGCA	GAGCAGGCCG	TTGGCAGGCA	ATCGACGTGC	TGCTCCGTGC
120	AAGGTGGGAG	GGCCCCGATC	CGGTGACCAT	AGCAGCTCCG	CCGCAGCTTC	GTGGCGGAGC
180	AACTTGGCAG	AAAGAAGGTG	GGGAACCGGG	GTATTTGAAG	CTCAGTGGAG	ATGCCATTCC
240	ACACCTGGCT	TGGGGCATTT	TTGGAGTCCC	GGTGTTTTGT	GGGCAAGAAA	AGCTGTTCAA



- (2) INFORMATION FOR SEQ ID NO: 6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 162 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Mouse
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ala Pro Ile Lys Val Gly Asp Ala Ile Pro Ser Val Glu Val Phe 1 5 10 15

Glu Gly Glu Pro Gly Lys Lys Val Asn Leu Ala Glu Leu Phe Lys Gly 20 25 30

Lys Lys Gly Val Leu Phe Gly Val Pro Gly Ala Phe Thr Pro Gly Cys 35 40 45

Ser Lys Thr His Leu Pro Gly Phe Val Glu Gln Ala Gly Ala Leu Lys 50 55 60

Ala Lys Gly Ala Gln Val Val Ala Cys Leu Ser Val Asn Asp Val Phe 65 70 75 80

Val Ile Glu Glu Trp Gly Arg Ala His Gln Ala Glu Gly Lys Val Arg 85 90 95

Leu Leu Ala Asp Pro Thr Gly Ala Phe Gly Lys Ala Thr Asp Leu Leu 100 105 110

Leu Asp Asp Ser Leu Val Ser Leu Phe Gly Asn Arg Arg Leu Lys Arg 115 120 125 Phe Ser Met Val Ile Asp Asn Gly Ile Val Lys Ala Leu Asn Val Glu 130 135 140

Pro Asp Gly Thr Gly Leu Thr Cys Ser Leu Ala Pro Asn Ile Leu Ser 145 150 155 160

Gln Leu

### (2) INFORMATION FOR SEQ ID NO: 7:

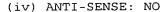
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 469 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 161..382
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

60 GGGTATGGGA CTAGCTGGCG TGTGCGCCCT GAGACGCTCA GCGGGCTATA TACTCGTCGG TGGGGCCGGC GGTCAGTCTG CGGCAGCGGC AGCAAGACGG TGCAGTGAAG GAGAGTGGGC 120 GTCTGGCGGG GTCCGCAGTT TCAGCAGAGC CGCTGCAGCC ATGGCCCCAA TCAAGGTTCG 180 GCTCCTGGCT GATCCCACTG GGGCCTTTGG GAAGGAGACA GACTTATTAC TAGATGATTC 240 GCTGGTGTCC ATCTTTGGGA ATCGACGTCT CAAGAGGTTC TCCATGGTGG TACAGGATGG 300 360 CATAGTGAAG GCCCTGAATG TGGAACCAGA TGGCACAGGC CTCACCTGCA GCCTGGCACC CAATATCATC TCACAGCTCT GAGGCCCTGG GCCAGATTAC TTCCTCCACC CCTCCCTATC 420 TCACCTGCCC AGCCGTGTGC TGGGGCCCTG CAATTGGAAT GTTGGCCAG 469

- (2) INFORMATION FOR SEQ ID NO: 8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 601 base pairs(B) TYPE: nucleic acid
    - (B) TIPE: Nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO

•





(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

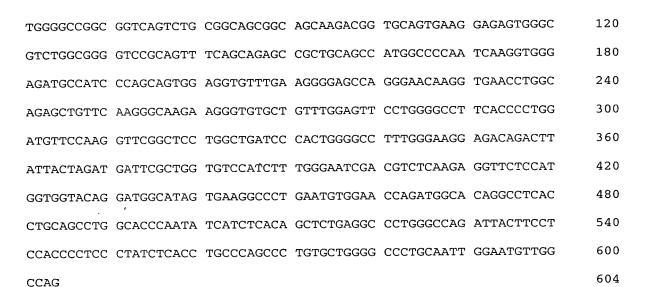
(B) LOCATION: 161..514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

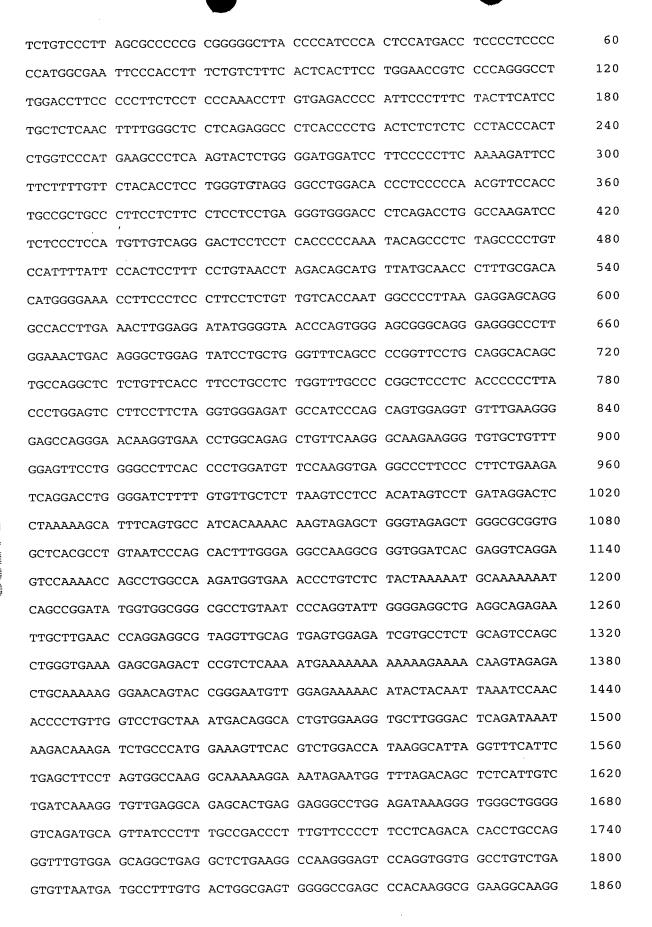
GGGTATGGGA	CTAGCTGGCG	TGTGCGCCCT	GAGACGCTCA	GCGGGCTATA	TACTCGTCGG	60
TGGGGCCGGC	GGTCAGTCTG	CGGCAGCGGC	AGCAAGACGG	TGCAGTGAAG	GAGAGTGGGC	120
GTCTGGCGGG	GTCCGCAGTT	TCAGCAGAGC	CGCTGCAGCC	ATGGCCCCAA	TCAAGACACA	180
CCTGCCAGGG	TTTGTGGAGC	AGGCTGAGGC	TCTGAAGGCC	AAGGGAGTCC	AGGTGGTGGC	240
CTGTCTGAGT	GTTAATGATG	CCTTTGTGAC	TGGCGAGTGG	GGCCGAGCCC	ACAAGGCGGA	300
AGGCAAGGTT	CGGCTCCTGG	CTGATCCCAC	TGGGGCCTTT	GGGAAGGAGA	CAGACTTATT	360
ACTAGATGAT	TCGCTGGTGT	CCATCTTTGG	GAATCGACGT	CTCAAGAGGT	TCTCCATGGT	420
GGTACAGGAT	GGCATAGTGA	AGGCCCTGAA	TGTGGAACCA	GATGGCACAG	GCCTCACCTG	480
CAGCCTGGCA	CCCAATATCA	TCTCACAGCT	CTGAGGCCCT	GGGCCAGATT	ACTTCCTCCA	540
CCCCTCCCTA	TCTCACCTGC	CCAGCCCTGT	GCTGGGGCCC	TGCAATTGGA	ATGTTGGCCA	600
G						601

# (2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 604 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 161..517
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:



- (2) INFORMATION FOR SEQ ID NO: 10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2710 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Homo sapiens
  - (ix) FEATURE:
    - (A) NAME/KEY: exon
    - (B) LOCATION: 2516..2710
  - (ix) FEATURE:
    - (A) NAME/KEY: exon
    - (B) LOCATION: 2074..2135
  - (ix) FEATURE:
    - (A) NAME/KEY: exon
    - (B) LOCATION: 1932... 1970
  - (ix) FEATURE:
    - (A) NAME/KEY: exon
    - (B) LOCATION: 1728..1859
  - (ix) FEATURE:
    - (A) NAME/KEY: exon
    - (B) LOCATION:802..936
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:



rgaggtgagg	GGCCTGCAGG	GAGTCAGGAC	CAGGTAGGAT	ATTCTTCTTG	TGACCTCTAC	1920
TTTCTCTGCA	GGTTCGGCTC	CTGGCTGATC	CCACTGGGGC	CTTTGGGAAG	GTGAGTGTTC	1980
CCCTGACCGC	CACAGGGACA	TGGCGGTGCG	GGGAGCAGTG	GGGGCCCTTG	GCCTCTTCAA	2040
GGATTTCTGA	CACTTTTCTC	TGTCTCTTCT	TAGGAGACAG	ACTTATTACT	AGATGATTCG	2100
CTGGTGTCCA	TCTTTGGGAA	TCGACGTCTC	AAGAGGTAAA	AGTGGAGAGT	CCTCTGTGGA	2160
GAAAGTCCTC	TGTGGGAGAG	AGTCCTCTGT	GGGAGAGAGT	CCTCTGTGGA	GAGGGTCCTC	2220
rgtgggaaga	GTCGTCTGTG	GGGGAGATGT	GTGGGAGAGA	GTCCTGTGTG	GGGAGAGTCT	2280
TCTGTAGGGG	AGAGTCCTCT	GGGGAGAGAG	TCCTGTGTGG	GGGAGAGTCC	TCTGTGGGGA	2340
GAGTCCTCTG	TGTGGAGAGA	GTCCTGTGTG	GTGGTGAGTC	CTCTGTGGGG	GAGAGTCCTC	2400
TGTGGGGGGA	GTCCTCTCTG	GAGTTCTCTT	GGGCCCCTGG	CTGTTCACTG	CCTGTCTCCA	2460
TGCCCAGCCT	CCAAGCCCAG	GCTGATGCAG	CTGGCTGGGC	CCCTCTTTCC	GGCAGGTTCT	2520
CCATGGTGGT	ACAGGATGGC	ATAGTGAAGG	CCCTGAATGT	GGAACCAGAT	GGCACAGGCC	2580
TCACCTGCAG	CCTGGCACCC	AATATCATCT	CACAGCTCTG	AGGCCCTGGG	CCAGATTACT	2640
TCCTCCACCC	CTCCCTATCT	CACCTGCCCA	GCCCTGTGCT	GGGGCCCTGC	AATTGGAATG	2700
TTGGCCAGAT						2710

- (2) INFORMATION FOR SEQ ID NO: 11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCATCCCAG CAGTGGAGGT GTTTG

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	
TTGAACAGCT CTGCCAGGTT CACC	24
(2) INFORMATION FOR SEQ ID NO: 13:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 24 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
TGGAGGTGTT TGAAGGGGAG CCAG	24
(2) INFORMATION FOR SEQ ID NO: 14:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 24 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
CAGGTTCACC TTGTTCCCTG GCTC	24
(2) INFORMATION FOR SEQ ID NO: 15:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 20 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:	
GGGTATGGGA CTAGCTGGCG	20
(2) INFORMATION FOR SEQ ID NO: 16:	_ •
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>	

	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:	
(	CTGGCCAACA TTCCAATTGC AG	22
	(2) INFORMATION FOR SEQ ID NO: 17:	
	<ul><li>(i) .SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 24 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(with grouping programmer), cro to No. 17.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:	24
	ATGTTATGCA ACCCTTTGCG ACAC	24
	(2) INFORMATION FOR SEQ ID NO: 18:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 24 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:	
	GTGTTTGAAG GGGAGCCAGG GAAC	24
	(2) INFORMATION FOR SEQ ID NO: 19:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 24 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
;	AGAGACAGGG TTTCACCATC TTGG	24
-	TOTAL	

(D) TOPOLOGY: linear